#/6

SEQUENCE LISTING

<110> Lowe, Keith S.
      Gordon-Kamm, William J.
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      Rasco-Gaunt, Sonriza
      Cahoon, Rebecca E.
      Sun, Xifan
      Hoester, George J.
      Gregory, Carolyn A.
      Nadimpalli, Ramgopal

<120> Transcriptional Activator Nucleic Acids,
      Polypeptides, and Methods of Use Thereof

<130> 0943

<140> 09/435,054
<141> 1999-11-08

<150> 60/107,643
<151> 1998-11-09

<160> 26

<170> FastSEQ for Windows Version 3.0

<210> 1
<211> 1173
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (69)...(902)

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gagagcca atg gac tcc agc agc ttc ctc cct gcc gcc ggc gcg gag aat     110
         Met Asp Ser Ser Ser Phe Leu Pro Ala Ala Gly Ala Glu Asn
          1               5                  10

ggc tcg gcg gcg ggc ggc gcc aac aat ggc ggc gct gct cag cag cat     158
Gly Ser Ala Ala Gly Gly Ala Asn Asn Gly Gly Ala Ala Gln Gln His
 15              20              25                     30

gcg gcg ccg gcg atc cgc gag cag gac cgg ctg atg ccg atc gcg aac     206
Ala Ala Pro Ala Ile Arg Glu Gln Asp Arg Leu Met Pro Ile Ala Asn
             35                  40                  45

gtg atc cgc atc atg cgg cgc gtg ctg ccg gcg cac gcc aag atc tcg     254
Val Ile Arg Ile Met Arg Arg Val Leu Pro Ala His Ala Lys Ile Ser
         50                  55                  60
```

1

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gac gac gcc aag gag acg atc cag gag tgc gtg tcg gag tac atc agc       302
Asp Asp Ala Lys Glu Thr Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser
        65              70                  75

ttc atc acg ggg gag gcc aac gag cgg tgc cag cgg gag cag cgc aag       350
Phe Ile Thr Gly Glu Ala Asn Glu Arg Cys Gln Arg Glu Gln Arg Lys
        80              85                  90

acc atc acc gcc gag gac gtg ctg tgg gcc atg agc cgc ctc ggc ttc       398
Thr Ile Thr Ala Glu Asp Val Leu Trp Ala Met Ser Arg Leu Gly Phe
95              100                 105                 110

gac gac tac gtc gag ccg ctc ggc gcc tac ctc cac cgc tac cgc gag       446
Asp Asp Tyr Val Glu Pro Leu Gly Ala Tyr Leu His Arg Tyr Arg Glu
                115                 120                 125

ttc gag ggc gac gcg cgc ggc gtc ggg ctc gtc ccg ggg gcc gcc cca       494
Phe Glu Gly Asp Ala Arg Gly Val Gly Leu Val Pro Gly Ala Ala Pro
            130                 135                 140

tcg cgc ggc ggc gac cac cac ccg cac tcc atg tcg cca gcg gcg atg       542
Ser Arg Gly Gly Asp His His Pro His Ser Met Ser Pro Ala Ala Met
            145                 150                 155

ctc aag tcc cgc ggg cca gtc tcc gga gcc gcc atg cta ccg cac cac       590
Leu Lys Ser Arg Gly Pro Val Ser Gly Ala Ala Met Leu Pro His His
        160                 165                 170

cac cac cac cac gac atg cag atg cac gcc gcc atg tac ggg gga acg       638
His His His His Asp Met Gln Met His Ala Ala Met Tyr Gly Gly Thr
175                 180                 185                 190

gcc gtg ccc ccg ccg gcc ggg cct cct cac cac ggc ggg ttc ctc atg       686
Ala Val Pro Pro Pro Ala Gly Pro Pro His His Gly Gly Phe Leu Met
                195                 200                 205

cca cac cca cag ggt agt agc cac tac ctg cct tac gcg tac gag ccc       734
Pro His Pro Gln Gly Ser Ser His Tyr Leu Pro Tyr Ala Tyr Glu Pro
                210                 215                 220

acg tac ggc ggt gag cac gcc atg gct gca tac tat gga ggc gcc gcg       782
Thr Tyr Gly Gly Glu His Ala Met Ala Ala Tyr Tyr Gly Gly Ala Ala
            225                 230                 235

tac gcg ccc ggc aac ggc ggg agc ggc gac ggc agt ggc agt ggc ggc       830
Tyr Ala Pro Gly Asn Gly Gly Ser Gly Asp Gly Ser Gly Ser Gly Gly
            240                 245                 250

ggt ggc ggg agc gcg tcg cac aca ccg cag ggc agc ggc ggc ttg gag       878
Gly Gly Gly Ser Ala Ser His Thr Pro Gln Gly Ser Gly Gly Leu Glu
255                 260                 265                 270

cac ccg cac ccg ttc gcg tac aag tagctagttc gtacgtcgtt cgacttgagc      932
His Pro His Pro Phe Ala Tyr Lys
            275
```

2

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aagccatcga tctgctgatc tgaacgtacg ctgtattgta cacgcatgca cgtacgtatc    992
ggcggctagc tctcctgttt aagttgtact gtgattctgt cccggccggc tagcaactta   1052
gtatcttcct tcagtctcta gtttcttagc agtcgtagaa gtgttcaatg cttgccagtg   1112
tgttgtttta gggccggggt aaaccatccg atgagattat ttcaaaaaaa aaaaaaaaa    1172
a                                                                    1173
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<210> 2
<211> 278
<212> PRT
<213> Zea mays

<400> 2

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Met Asp Ser Ser Ser Phe Leu Pro Ala Ala Gly Ala Glu Asn Gly Ser
 1               5                  10                  15
Ala Ala Gly Gly Ala Asn Asn Gly Gly Ala Ala Gln Gln His Ala Ala
            20                  25                  30
Pro Ala Ile Arg Glu Gln Asp Arg Leu Met Pro Ile Ala Asn Val Ile
        35                  40                  45
Arg Ile Met Arg Arg Val Leu Pro Ala His Ala Lys Ile Ser Asp Asp
    50                  55                  60
Ala Lys Glu Thr Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Ile
65                  70                  75                  80
Thr Gly Glu Ala Asn Glu Arg Cys Gln Arg Glu Gln Arg Lys Thr Ile
                85                  90                  95
Thr Ala Glu Asp Val Leu Trp Ala Met Ser Arg Leu Gly Phe Asp Asp
            100                 105                 110
Tyr Val Glu Pro Leu Gly Ala Tyr Leu His Arg Tyr Arg Glu Phe Glu
        115                 120                 125
Gly Asp Ala Arg Gly Val Gly Leu Val Pro Gly Ala Ala Pro Ser Arg
    130                 135                 140
Gly Gly Asp His His Pro His Ser Met Ser Pro Ala Ala Met Leu Lys
145                 150                 155                 160
Ser Arg Gly Pro Val Ser Gly Ala Ala Met Leu Pro His His His His
                165                 170                 175
His His Asp Met Gln Met His Ala Ala Met Tyr Gly Gly Thr Ala Val
            180                 185                 190
Pro Pro Pro Ala Gly Pro Pro His His Gly Gly Phe Leu Met Pro His
        195                 200                 205
Pro Gln Gly Ser Ser His Tyr Leu Pro Tyr Ala Tyr Glu Pro Thr Tyr
    210                 215                 220
Gly Gly Glu His Ala Met Ala Ala Tyr Tyr Gly Gly Ala Ala Tyr Ala
225                 230                 235                 240
Pro Gly Asn Gly Gly Ser Gly Asp Gly Ser Gly Ser Gly Gly Gly Gly
                245                 250                 255
Gly Ser Ala Ser His Thr Pro Gln Gly Ser Gly Gly Leu Glu His Pro
            260                 265                 270
His Pro Phe Ala Tyr Lys
        275
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<210> 3
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<212> DNA
<213> Artificial Sequence

<220>
<223> primer

3

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tagtagcgag agccaatgga   20

<210> 4
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 4
gccgggacag aatcacagta   20

<210> 5
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 5
tagtagcgag agccaatgga   20

<210> 6
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 6
cccggcccta aaacaacaca   20

<210> 7
<211> 481
<212> DNA
<213> Argemone mexicana

<220>
<221> CDS
<222> (44)...(481)

<221> misc_feature
<222> (1)...(481)
<223> n = A,T,C or G

<400> 7
cgagagaaag agttggtgaa gaagaagaag aagttgaaaa gag atg gaa cgt ggt   55
                                                   Met Glu Arg Gly
                                                   1

ggt ggt ggt ggt ggt agt ggt ggt ggt ttc cat gga tat cag aaa ctc   103

4

```
Gly Gly Gly Gly Gly Ser Gly Gly Gly Phe His Gly Tyr Gln Lys Leu
 5                  10                  15                  20

cca aaa tca aac tcc gct gga atg atg ctc tcg gag cta tcg aat aac     151
Pro Lys Ser Asn Ser Ala Gly Met Met Leu Ser Glu Leu Ser Asn Asn
                    25                  30                  35

aac aac aat att gac gta aac tct aca tgt act gta cga gag caa gat     199
Asn Asn Asn Ile Asp Val Asn Ser Thr Cys Thr Val Arg Glu Gln Asp
                40                  45                  50

cga tac atg cca att gct aat gtg atc agg atc atg cgt aag gta ctt     247
Arg Tyr Met Pro Ile Ala Asn Val Ile Arg Ile Met Arg Lys Val Leu
                55                  60                  65

cct act cat gcc aag atc tct gac gat gcc aaa gaa act atc caa gaa     295
Pro Thr His Ala Lys Ile Ser Asp Asp Ala Lys Glu Thr Ile Gln Glu
                70                  75                  80

tgt gtc tca gaa tac atc agt ttc atc aca agt gaa gcc aat gat cgt     343
Cys Val Ser Glu Tyr Ile Ser Phe Ile Thr Ser Glu Ala Asn Asp Arg
 85                  90                  95                 100

tgc caa cgt gaa caa aga aag aca atc aca gct gaa gat gtt tta tgg     391
Cys Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp Val Leu Trp
                105                 110                 115

gcg atg agc aaa cta ggg ntt gat gag tac att gaa cct cta act ctt     439
Ala Met Ser Lys Leu Gly Xaa Asp Glu Tyr Ile Glu Pro Leu Thr Leu
                120                 125                 130

tac ctt caa cgt tat cgt gag ttt gaa ggt gna cgt tgg tca             481
Tyr Leu Gln Arg Tyr Arg Glu Phe Glu Gly Xaa Arg Trp Ser
                135                 140                 145
```

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<210> 8
<211> 146
<212> PRT
<213> Argemone mexicana

<220>
<221> VARIANT
<222> (1)...(146)
<223> Xaa = Any Amino Acid

<400> 8
Met Glu Arg Gly Gly Gly Gly Gly Gly Ser Gly Gly Gly Phe His Gly
 1               5                  10                  15
Tyr Gln Lys Leu Pro Lys Ser Asn Ser Ala Gly Met Met Leu Ser Glu
                20                  25                  30
Leu Ser Asn Asn Asn Asn Asn Ile Asp Val Asn Ser Thr Cys Thr Val
            35                  40                  45
Arg Glu Gln Asp Arg Tyr Met Pro Ile Ala Asn Val Ile Arg Ile Met
        50                  55                  60
Arg Lys Val Leu Pro Thr His Ala Lys Ile Ser Asp Asp Ala Lys Glu
```

```
            65                      70                       75                         80
Thr Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Ile Thr Ser Glu
                        85                      90                          95
Ala Asn Asp Arg Cys Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu
                100                         105                         110
Asp Val Leu Trp Ala Met Ser Lys Leu Gly Xaa Asp Glu Tyr Ile Glu
                    115                         120                         125
Pro Leu Thr Leu Tyr Leu Gln Arg Tyr Arg Glu Phe Glu Gly Xaa Arg
                130                         135                         140
Trp Ser
145
```

        <210> 9
        <211> 942
        <212> DNA
        <213> Glycine max

        <220>
        <221> CDS
        <222> (3)...(722)

        <400> 9

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gc acg agc tct ctt ata atc aca cac aca cct acc tta ata gct atg       47
   Thr Ser Ser Leu Ile Ile Thr His Thr Pro Thr Leu Ile Ala Met
   1               5                   10                      15

gaa act gga ggc ttt cac ggc tac cgc aag ctc ccc aac acc acc gct      95
Glu Thr Gly Gly Phe His Gly Tyr Arg Lys Leu Pro Asn Thr Thr Ala
                    20                  25                  30

ggg ttg aag ctg tca gtg tca gac atg aac atg agg cag cag gta gca     143
Gly Leu Lys Leu Ser Val Ser Asp Met Asn Met Arg Gln Gln Val Ala
                35                  40                  45

tca tca gat cac agt gca gcc aca gga gag gag aac gaa tgc acg gtg     191
Ser Ser Asp His Ser Ala Ala Thr Gly Glu Glu Asn Glu Cys Thr Val
            50                  55                  60

agg gag caa gac agg ttc atg cca atc gcc aac gtg att agg atc atg     239
Arg Glu Gln Asp Arg Phe Met Pro Ile Ala Asn Val Ile Arg Ile Met
        65                  70                  75

cgc aag att ctc cct cca cac gca aaa atc tcg gac gat gca aaa gaa     287
Arg Lys Ile Leu Pro Pro His Ala Lys Ile Ser Asp Asp Ala Lys Glu
80                  85                  90                  95

aca atc caa gag tgc gtg tct gag tac atc agc ttc atc aca ggt gag     335
Thr Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Ile Thr Gly Glu
                    100                 105                 110

gcg aac gag cgt tgc cag agg gag cag cgg aag acc ata acc gca gag     383
Ala Asn Glu Arg Cys Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu
                    115                 120                 125

gac gtg ctt tgg gcc atg agc aag ctt gga ttc gac gac tac atc gaa     431
Asp Val Leu Trp Ala Met Ser Lys Leu Gly Phe Asp Asp Tyr Ile Glu
```

6

```
ccg ttg acc atg tac ctt cac cgc tac cgt gaa ctt gag ggt gac cgc    479
Pro Leu Thr Met Tyr Leu His Arg Tyr Arg Glu Leu Glu Gly Asp Arg
    145                 150                 155

acc tct atg agg ggt gaa cca ctc ggg aag agg act gtg gaa tac gcc    527
Thr Ser Met Arg Gly Glu Pro Leu Gly Lys Arg Thr Val Glu Tyr Ala
160                 165                 170                 175

acg ctt ggt gtt gct act gct ttt gtc cct cca ccc tat cat cac cac    575
Thr Leu Gly Val Ala Thr Ala Phe Val Pro Pro Pro Tyr His His His
            180                 185                 190

aat ggg tac ttt ggt gct gcc atg ccc atg ggg act tac gtt agg gaa    623
Asn Gly Tyr Phe Gly Ala Ala Met Pro Met Gly Thr Tyr Val Arg Glu
            195                 200                 205

gcg cca cca aat aca gcc tcc tcc cat cac cac cac cac cac cac cac    671
Ala Pro Pro Asn Thr Ala Ser Ser His His His His His His His His
        210                 215                 220

cac cat gct cgt gga atc tcc aat gct cat gaa cca aat gct cgc tcc    719
His His Ala Arg Gly Ile Ser Asn Ala His Glu Pro Asn Ala Arg Ser
    225                 230                 235

ata taaaattata taattatgac taggattcag aacaagactt gatgatgatt         772
Ile
240

agcttaactc tcagtaattg gtgctagagt actactgttg ttgaggatac tttattttat    832
aattaagggc tgggaaggga gttagtatat tcctaatcct aactatgtgc atctttaatt    892
tatgaaatca ctttgtttta accttgatg aaaaaaaaaa aaaaaaaaaa               942
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<210> 10
<211> 240
<212> PRT
<213> Glycine max

<400> 10

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Thr Ser Ser Leu Ile Ile Thr His Thr Pro Thr Leu Ile Ala Met Glu
1               5                   10                  15
Thr Gly Gly Phe His Gly Tyr Arg Lys Leu Pro Asn Thr Thr Ala Gly
            20                  25                  30
Leu Lys Leu Ser Val Ser Asp Met Asn Met Arg Gln Gln Val Ala Ser
        35                  40                  45
Ser Asp His Ser Ala Ala Thr Gly Glu Glu Asn Glu Cys Thr Val Arg
    50                  55                  60
Glu Gln Asp Arg Phe Met Pro Ile Ala Asn Val Ile Arg Ile Met Arg
65                  70                  75                  80
Lys Ile Leu Pro Pro His Ala Lys Ile Ser Asp Asp Ala Lys Glu Thr
            85                  90                  95
Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Ile Thr Gly Glu Ala
            100                 105                 110
Asn Glu Arg Cys Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp
        115                 120                 125
```

7

```
Val Leu Trp Ala Met Ser Lys Leu Gly Phe Asp Asp Tyr Ile Glu Pro
    130                 135                 140
Leu Thr Met Tyr Leu His Arg Tyr Arg Glu Leu Glu Gly Asp Arg Thr
145                 150                 155                 160
Ser Met Arg Gly Glu Pro Leu Gly Lys Arg Thr Val Glu Tyr Ala Thr
                165                 170                 175
Leu Gly Val Ala Thr Ala Phe Val Pro Pro Pro Tyr His His His Asn
            180                 185                 190
Gly Tyr Phe Gly Ala Ala Met Pro Met Gly Thr Tyr Val Arg Glu Ala
        195                 200                 205
Pro Pro Asn Thr Ala Ser Ser His His His His His His His His His
    210                 215                 220
His Ala Arg Gly Ile Ser Asn Ala His Glu Pro Asn Ala Arg Ser Ile
225                 230                 235                 240
```

<210> 11
<211> 905
<212> DNA
<213> Veronia   mespilifolia

<220>
<221> CDS
<222> (58)...(699)

<400> 11

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                                                                    Met
                                                                    1

gaa cgt gga gga ggt ttc cat ggc tac cac agg ctc ccc atc cac cct          108
Glu Arg Gly Gly Gly Phe His Gly Tyr His Arg Leu Pro Ile His Pro
        5                   10                  15

aca tct gga atc caa caa tcg gat atg aag cta aag cta cca gaa atg          156
Thr Ser Gly Ile Gln Gln Ser Asp Met Lys Leu Lys Leu Pro Glu Met
        20                  25                  30

acc aac aat aac tcg tcc act gat gac aat gag tgc acc gtt cga gaa          204
Thr Asn Asn Asn Ser Ser Thr Asp Asp Asn Glu Cys Thr Val Arg Glu
        35                  40                  45

cag gac cgc ttc atg ccg ata gca aac gtg atc cgc atc atg cgg aag          252
Gln Asp Arg Phe Met Pro Ile Ala Asn Val Ile Arg Ile Met Arg Lys
    50                  55                  60                  65

atc ctt cct cca cat gcc aag atc tct gat gat gcc aaa gag acg atc          300
Ile Leu Pro Pro His Ala Lys Ile Ser Asp Asp Ala Lys Glu Thr Ile
                70                  75                  80

caa gaa tgt gtt tca gag tac att agc ttt gtc aca ggc gag gca aat          348
Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Val Thr Gly Glu Ala Asn
                85                  90                  95

gac cgc tgc cag cgt gag caa agg aag acc atc aca gct gaa gat gtg          396
Asp Arg Cys Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp Val
        100                 105                 110
```

8

```
ctc tgg gct atg agc aaa ctg gga ttt gat gat tat atc gag ccc ttg      444
Leu Trp Ala Met Ser Lys Leu Gly Phe Asp Asp Tyr Ile Glu Pro Leu
    115             120                 125

act gtg tat ctc cat cgc tac agg gag ttt gat ggt ggc gaa cgt gga      492
Thr Val Tyr Leu His Arg Tyr Arg Glu Phe Asp Gly Gly Glu Arg Gly
130             135                 140                 145

tcc ata agg ggt gag ccc ctt gtg aag agg agt act tct gat cct ggt      540
Ser Ile Arg Gly Glu Pro Leu Val Lys Arg Ser Thr Ser Asp Pro Gly
            150                 155                 160

cac ttt ggg atg gct tct ttt gtg cct gct ttt cat atg ggt cat cat      588
His Phe Gly Met Ala Ser Phe Val Pro Ala Phe His Met Gly His His
            165                 170                 175

aac ggc ttc ttt ggt cct gca agc att ggt ggt ttc ctg aaa gac cca      636
Asn Gly Phe Phe Gly Pro Ala Ser Ile Gly Gly Phe Leu Lys Asp Pro
            180                 185                 190

tcg agt gct ggc cct tcg gga cct gca gtc gct ggg ttt gag ccg tat      684
Ser Ser Ala Gly Pro Ser Gly Pro Ala Val Ala Gly Phe Glu Pro Tyr
    195                 200                 205

gct cag tgt aaa gag taactgcaaa aagtaggggt tgggatgaga tgatgatgat     739
Ala Gln Cys Lys Glu
210


ggtggtggtg gtggtggttt gttttgtttt gttctttctt ttttttttct tctttctttt     799
cttggtcatt gaggaacaaa cttacattgg ttcactttgg ctaggcatgt aaacggttaa     859
catgcttatc aagtagtagt tttcgatcaa aaaaaaaaaa aaaaaa                     905

        <210> 12
        <211> 214
        <212> PRT
        <213> Veronia  mespilifolia

        <400> 12
Met Glu Arg Gly Gly Gly Phe His Gly Tyr His Arg Leu Pro Ile His
1               5                   10                  15
Pro Thr Ser Gly Ile Gln Gln Ser Asp Met Lys Leu Lys Leu Pro Glu
            20                  25                  30
Met Thr Asn Asn Asn Ser Ser Thr Asp Asp Asn Glu Cys Thr Val Arg
        35                  40                  45
Glu Gln Asp Arg Phe Met Pro Ile Ala Asn Val Ile Arg Ile Met Arg
    50                  55                  60
Lys Ile Leu Pro Pro His Ala Lys Ile Ser Asp Asp Ala Lys Glu Thr
65                  70                  75                  80
Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Val Thr Gly Glu Ala
                85                  90                  95
Asn Asp Arg Cys Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp
            100                 105                 110
Val Leu Trp Ala Met Ser Lys Leu Gly Phe Asp Asp Tyr Ile Glu Pro
    115                 120                 125
Leu Thr Val Tyr Leu His Arg Tyr Arg Glu Phe Asp Gly Gly Glu Arg
```

9

```
            130                      135                      140
Gly Ser Ile Arg Gly Glu Pro Leu Val Lys Arg Ser Thr Ser Asp Pro
145                           150                      155                      160
Gly His Phe Gly Met Ala Ser Phe Val Pro Ala Phe His Met Gly His
                    165                      170                      175
His Asn Gly Phe Phe Gly Pro Ala Ser Ile Gly Gly Phe Leu Lys Asp
               180                      185                      190
Pro Ser Ser Ala Gly Pro Ser Gly Pro Ala Val Ala Gly Phe Glu Pro
          195                      200                      205
Tyr Ala Gln Cys Lys Glu
     210


     <210> 13
     <211> 763
     <212> DNA
     <213> Zea mays

     <220>
     <221> CDS
     <222> (1)...(480)

     <400> 13
gca cga ggc aag acc gtc acc tcc gag gac atc gtg tgg gcc atg agc        48
Ala Arg Gly Lys Thr Val Thr Ser Glu Asp Ile Val Trp Ala Met Ser
1                   5                        10                      15

cgc ctc ggc ttc gac gac tac gtc gcg ccc ctc ggc gcc ttc ctc cag       96
Arg Leu Gly Phe Asp Asp Tyr Val Ala Pro Leu Gly Ala Phe Leu Gln
                    20                      25                      30

cgc atg cgc gac gac agc gac cac ggc ggt gaa gag cgc ggc ggc cct      144
Arg Met Arg Asp Asp Ser Asp His Gly Gly Glu Glu Arg Gly Gly Pro
               35                      40                      45

gca ggg cgt ggt ggc tcg cgc cgc ggc tcg tcg tcc ttg ccg ctc cac      192
Ala Gly Arg Gly Gly Ser Arg Arg Gly Ser Ser Ser Leu Pro Leu His
          50                      55                      60

tgc ccg cag cag atg cac cac ctg cac cca gcc gtc tgc cgg cgt ccg      240
Cys Pro Gln Gln Met His His Leu His Pro Ala Val Cys Arg Arg Pro
65                      70                      75                      80

cac cag agc gtg tcg cct gct gca gga tac gcc gtc cgg ccc gtt ccc      288
His Gln Ser Val Ser Pro Ala Ala Gly Tyr Ala Val Arg Pro Val Pro
                         85                      90                      95

cgc ccg atg cca gcc cgt ggg tac cgc atg cag ggc gga gac cac cgc      336
Arg Pro Met Pro Ala Arg Gly Tyr Arg Met Gln Gly Gly Asp His Arg
                    100                     105                     110

agc gtg ggc ggc gtg gct ccc tgc agc tac gga ggg gcg ctc gtc cag      384
Ser Val Gly Gly Val Ala Pro Cys Ser Tyr Gly Gly Ala Leu Val Gln
               115                     120                     125

gcc ggt gga acc caa cac gtt gtt gga ttc cac gac gac gag gca agc      432
Ala Gly Gly Thr Gln His Val Val Gly Phe His Asp Asp Glu Ala Ser
```

```
                130                    135                        140
tct tcg agt gaa aat ccg ccg ccg gag ggg cgt gcc gct ggc tcg aac        480
Ser Ser Ser Glu Asn Pro Pro Pro Glu Gly Arg Ala Ala Gly Ser Asn
145                    150                     155                160

tagcctagct tctcagttcc ccgtgtacaa taagaggggc ggtcgcggcg ccgcgccgcg     540
cccttgggtt gggccggggcg ctatgctgca gtttggtttg taaactaacg agcctagggt    600
agctggtgca cgcgcgccac ctcgccggac gtcgccgtcg tcgtcggcat ggacttaacc     660
ggcgggccct gttgttattt ctcaagtttg tagccaacgc actgttcggt gcgttccata     720
atttaattta ccatgttgct ctcgaaaaaa aaaaaaaaaa aaa                       763

        <210> 14
        <211> 160
        <212> PRT
        <213> Zea mays

        <400> 14
Ala Arg Gly Lys Thr Val Thr Ser Glu Asp Ile Val Trp Ala Met Ser
1               5                   10                  15
Arg Leu Gly Phe Asp Asp Tyr Val Ala Pro Leu Gly Ala Phe Leu Gln
            20                  25                  30
Arg Met Arg Asp Asp Ser Asp His Gly Gly Glu Glu Arg Gly Gly Pro
        35                  40                  45
Ala Gly Arg Gly Gly Ser Arg Arg Gly Ser Ser Ser Leu Pro Leu His
    50                  55                  60
Cys Pro Gln Gln Met His His Leu His Pro Ala Val Cys Arg Arg Pro
65              70                  75                  80
His Gln Ser Val Ser Pro Ala Ala Gly Tyr Ala Val Arg Pro Val Pro
                85                  90                  95
Arg Pro Met Pro Ala Arg Gly Tyr Arg Met Gln Gly Gly Asp His Arg
            100                 105                 110
Ser Val Gly Gly Val Ala Pro Cys Ser Tyr Gly Gly Ala Leu Val Gln
            115                 120                 125
Ala Gly Gly Thr Gln His Val Val Gly Phe His Asp Asp Glu Ala Ser
    130                 135                 140
Ser Ser Ser Glu Asn Pro Pro Pro Glu Gly Arg Ala Ala Gly Ser Asn
145                 150                 155                 160

        <210> 15
        <211> 622
        <212> DNA
        <213> Zea mays

        <220>
        <221> CDS
        <222> (3)...(622)

        <221> misc_feature
        <222> (1)...(622)
        <223> n = A,T,C or G

        <400> 15
gc atg aat aat ccc caa aac cct aaa gcc agt gct cct tgc acc ttg         47
   Met Asn Asn Pro Gln Asn Pro Lys Ala Ser Ala Pro Cys Thr Leu
   1               5                   10                  15
```

11

```
cca ccg gag ctt ccc aaa gaa gca gtg gcg acc gac gaa gca ccg ccg       95
Pro Pro Glu Leu Pro Lys Glu Ala Val Ala Thr Asp Glu Ala Pro Pro
            20                  25                  30

cca atg ggc aac aac aac aac acg gaa tcg gcg acg gcg acg atg gtc       143
Pro Met Gly Asn Asn Asn Asn Thr Glu Ser Ala Thr Ala Thr Met Val
            35                  40                  45

cgg gag cag gac cgg ctg atg ccc gtg gcc aac gtg tcc cgc atc atg      191
Arg Glu Gln Asp Arg Leu Met Pro Val Ala Asn Val Ser Arg Ile Met
            50                  55                  60

cgc caa gtg ctg cct ccg tac gcc aag atc tcc gac gac gcc can gaa      239
Arg Gln Val Leu Pro Pro Tyr Ala Lys Ile Ser Asp Asp Ala Xaa Glu
        65                  70                  75

gtn atc caa gaa ttg ctn ttc gga att tca tca ctt ncg tcc tgg cga      287
Xaa Ile Gln Glu Leu Xaa Phe Gly Ile Ser Ser Leu Xaa Ser Trp Arg
    80                  85                  90                  95

ggc gaa acg aag cgg tgc cac acc gag cgc cgc aag acc gtc acc tcc      335
Gly Glu Thr Lys Arg Cys His Thr Glu Arg Arg Lys Thr Val Thr Ser
                100                 105                 110

gaa gac atc gtg tgg gcc atg agc cgc ctc ggc ttc gac gac tac gtc      383
Glu Asp Ile Val Trp Ala Met Ser Arg Leu Gly Phe Asp Asp Tyr Val
                115                 120                 125

gcg ccc ctc ggc gcc ttc ctc cag cgc atg cgc gac nac agc gaa cac      431
Ala Pro Leu Gly Ala Phe Leu Gln Arg Met Arg Asp Xaa Ser Glu His
            130                 135                 140

ggg ggt gaa aac gcg gcg gcc tgc ang ggg tng tgg tcn cgc cgc ggg      479
Gly Gly Glu Asn Ala Ala Ala Cys Xaa Gly Xaa Trp Xaa Arg Arg Gly
    145                 150                 155

tcg tct nct tgg cgc tcc ctt gcc gca ana gat gac aac ttg cac caa      527
Ser Ser Xaa Trp Arg Ser Leu Ala Ala Xaa Asp Asp Asn Leu His Gln
160                 165                 170                 175

acg tct gcc ggg ntc gga cca aaa ctn ttc cct gtt gca gga ata ccc      575
Thr Ser Ala Gly Xaa Gly Pro Lys Xaa Phe Pro Val Ala Gly Ile Pro
            180                 185                 190

gtc cng ggc cnt tcc ccc ccn aat cca acc att tgg ttt ccc ctt gc       622
Val Xaa Gly Xaa Ser Pro Xaa Asn Pro Thr Ile Trp Phe Pro Leu
        195                 200                 205


        <210> 16
        <211> 206
        <212> PRT
        <213> Zea mays

        <220>
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12

<221> VARIANT
<222> (1)...(206)
<223> Xaa = Any Amino Acid

<400> 16
Met Asn Asn Pro Gln Asn Pro Lys Ala Ser Ala Pro Cys Thr Leu Pro
1   5   10   15
Pro Glu Leu Pro Lys Glu Ala Val Ala Thr Asp Glu Ala Pro Pro Pro
            20   25   30
Met Gly Asn Asn Asn Asn Thr Glu Ser Ala Thr Ala Thr Met Val Arg
        35   40   45
Glu Gln Asp Arg Leu Met Pro Val Ala Asn Val Ser Arg Ile Met Arg
        50   55   60
Gln Val Leu Pro Pro Tyr Ala Lys Ile Ser Asp Asp Ala Xaa Glu Xaa
65   70   75   80
Ile Gln Glu Leu Xaa Phe Gly Ile Ser Ser Leu Xaa Ser Trp Arg Gly
                85   90   95
Glu Thr Lys Arg Cys His Thr Glu Arg Arg Lys Thr Val Thr Ser Glu
            100   105   110
Asp Ile Val Trp Ala Met Ser Arg Leu Gly Phe Asp Asp Tyr Val Ala
            115   120   125
Pro Leu Gly Ala Phe Leu Gln Arg Met Arg Asp Xaa Ser Glu His Gly
        130   135   140
Gly Glu Asn Ala Ala Ala Cys Xaa Gly Xaa Trp Xaa Arg Arg Gly Ser
145   150   155   160
Ser Xaa Trp Arg Ser Leu Ala Ala Xaa Asp Asp Asn Leu His Gln Thr
                165   170   175
Ser Ala Gly Xaa Gly Pro Lys Xaa Phe Pro Val Ala Gly Ile Pro Val
                180   185   190
Xaa Gly Xaa Ser Pro Xaa Asn Pro Thr Ile Trp Phe Pro Leu
                195   200   205

<210> 17
<211> 1121
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (3)...(1121)

<400> 17
gc acg agg gaa act gga ggc ttt cat ggc tac cgc aag ctc ccc aac   47
   Thr Arg Glu Thr Gly Gly Phe His Gly Tyr Arg Lys Leu Pro Asn
   1   5   10   15

aca acc tct ggg ttg aag ctg tca gtg tca gac atg aac atg aac atg   95
Thr Thr Ser Gly Leu Lys Leu Ser Val Ser Asp Met Asn Met Asn Met
                20   25   30

agg cag cag cag gta gca tca tca gat cag aac tgc agc aac cac agt   143
Arg Gln Gln Gln Val Ala Ser Ser Asp Gln Asn Cys Ser Asn His Ser
            35   40   45

gca gca gga gag gag aac gaa tgc acg gtg agg gag caa gac agg ttc   191
Ala Ala Gly Glu Glu Asn Glu Cys Thr Val Arg Glu Gln Asp Arg Phe

```
atg cca atc gct aac gtg ata cgg atc atg cgc aag att ctc cct cca      239
Met Pro Ile Ala Asn Val Ile Arg Ile Met Arg Lys Ile Leu Pro Pro
        65                  70                  75

cac gca aaa atc tcc gat gat gca aag gag aca atc caa gag tgc gtg      287
His Ala Lys Ile Ser Asp Asp Ala Lys Glu Thr Ile Gln Glu Cys Val
    80                  85                  90                  95

tcg gag tac atc agc ttc atc acc ggg gag gcc aac gag cgt tgc cag      335
Ser Glu Tyr Ile Ser Phe Ile Thr Gly Glu Ala Asn Glu Arg Cys Gln
                100                 105                 110

agg gag cag cgc aag acc ata acc gca gag gac gtg ctt tgg gca atg      383
Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp Val Leu Trp Ala Met
                115                 120                 125

agt aag ctt gga ttc gac gac tac atc gaa ccg tta acc atg tac ctt      431
Ser Lys Leu Gly Phe Asp Asp Tyr Ile Glu Pro Leu Thr Met Tyr Leu
                130                 135                 140

cac cgc tac cgt gag ctg gag ggt gac cgc acc tct atg agg ggt gaa      479
His Arg Tyr Arg Glu Leu Glu Gly Asp Arg Thr Ser Met Arg Gly Glu
            145                 150                 155

ccg ctc ggg aag agg act gtg gaa tat gcc acg ctt gct act gct ttt      527
Pro Leu Gly Lys Arg Thr Val Glu Tyr Ala Thr Leu Ala Thr Ala Phe
160                 165                 170                 175

gtg ccg cca ccc ttt cat cac cac aat ggc tac ttt ggt gct gcc atg      575
Val Pro Pro Pro Phe His His His Asn Gly Tyr Phe Gly Ala Ala Met
                180                 185                 190

ccc atg ggg act tac gtt agg gaa acg cca cca aat gct gcg tca tct      623
Pro Met Gly Thr Tyr Val Arg Glu Thr Pro Pro Asn Ala Ala Ser Ser
            195                 200                 205

cat cac cat cat gga atc tcc aat gct cat gaa cca aat gct cgc tcc      671
His His His His Gly Ile Ser Asn Ala His Glu Pro Asn Ala Arg Ser
        210                 215                 220

ata taa aat taa tga aga gta ctg ttc agt agg aga aca aga ctt ctt      719
Ile  *  Asn  *   *  Arg Val Leu Phe Ser Arg Arg Thr Arg Leu Leu
        225                 230                 235

gga ctt gat tag ctt aac tct cag tga ttg gtg tta gag tac tgt tgt      767
Gly Leu Asp  *  Leu Asn Ser Gln  *  Leu Val Leu Glu Tyr Cys Cys
                240                 245                 250

tga gga tgg tta att tta taa tta agg gct ggg aat tgg gga gtt agt      815
 *  Gly Trp Leu Ile Leu  *  Leu Arg Ala Gly Asn Trp Gly Val Ser
                255                 260

ata tat tcc taa tcc taa tta tgt gca tct tta att tat gga ata act      863
Ile Tyr Ser  *  Ser  *  Leu Cys Ala Ser Leu Ile Tyr Gly Ile Thr
```

```
ttg ttt ttt gtt tta act tct gat aat ttg gat ttt ctg atg ttt aat    911
Leu Phe Phe Val Leu Thr Ser Asp Asn Leu Asp Phe Leu Met Phe Asn
        280             285                 290

gtg gtt ttg tct atc cct tat taa cag tgc caa gct taa ggt ttt agc    959
Val Val Leu Ser Ile Pro Tyr  *  Gln Cys Gln Ala  *  Gly Phe Ser
295             300                 305

cat gct cca aaa tgg aat act tgt act gtt atg ttg ttc tgg tag tga   1007
His Ala Pro Lys Trp Asn Thr Cys Thr Val Met Leu Phe Trp  *   *
        310             315                 320

tgg tga tga aac ctg caa gtt atg ttt atg tat aaa gcc act att gat   1055
Trp  *   *  Asn Leu Gln Val Met Phe Met Tyr Lys Ala Thr Ile Asp
                325             330                 335

caa aat tag aga aat tat cat tta ata agt atc ctc cca tgt taa ttt   1103
Gln Asn  *  Arg Asn Tyr His Leu Ile Ser Ile Leu Pro Cys  *  Phe
            340             345                 350

taa aaa aaa aaa aaa aaa                                            1121
 *  Lys Lys Lys Lys Lys
            355
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<210> 18
<211> 355
<212> PRT
<213> Glycine max

<400> 18
Thr Arg Glu Thr Gly Gly Phe His Gly Tyr Arg Lys Leu Pro Asn Thr
1               5               10                  15
Thr Ser Gly Leu Lys Leu Ser Val Ser Asp Met Asn Met Asn Met Arg
        20                  25                  30
Gln Gln Gln Val Ala Ser Ser Asp Gln Asn Cys Ser Asn His Ser Ala
        35                  40                  45
Ala Gly Glu Glu Asn Glu Cys Thr Val Arg Glu Gln Asp Arg Phe Met
        50                  55                  60
Pro Ile Ala Asn Val Ile Arg Ile Met Arg Lys Ile Leu Pro Pro His
65                  70                  75                  80
Ala Lys Ile Ser Asp Asp Ala Lys Glu Thr Ile Gln Glu Cys Val Ser
            85                  90                  95
Glu Tyr Ile Ser Phe Ile Thr Gly Glu Ala Asn Glu Arg Cys Gln Arg
            100                 105                 110
Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp Val Leu Trp Ala Met Ser
            115                 120                 125
Lys Leu Gly Phe Asp Asp Tyr Ile Glu Pro Leu Thr Met Tyr Leu His
            130                 135                 140
Arg Tyr Arg Glu Leu Glu Gly Asp Arg Thr Ser Met Arg Gly Glu Pro
145                 150                 155                 160
Leu Gly Lys Arg Thr Val Glu Tyr Ala Thr Leu Ala Thr Ala Phe Val
                165                 170                 175
Pro Pro Pro Phe His His His Asn Gly Tyr Phe Gly Ala Ala Met Pro
```

```
                    180                    185                    190
      Met Gly Thr Tyr Val Arg Glu Thr Pro Pro Asn Ala Ala Ser Ser His
              195                    200                    205
      His His His Gly Ile Ser Asn Ala His Glu Pro Asn Ala Arg Ser Ile
              210                    215                    220
      Asn Arg Val Leu Phe Ser Arg Arg Thr Arg Leu Leu Gly Leu Asp Leu
      225                    230                    235                    240
      Asn Ser Gln Leu Val Leu Glu Tyr Cys Cys Gly Trp Leu Ile Leu Leu
                    245                    250                    255
      Arg Ala Gly Asn Trp Gly Val Ser Ile Tyr Ser Ser Leu Cys Ala Ser
              260                    265                    270
      Leu Ile Tyr Gly Ile Thr Leu Phe Phe Val Leu Thr Ser Asp Asn Leu
              275                    280                    285
      Asp Phe Leu Met Phe Asn Val Val Leu Ser Ile Pro Tyr Gln Cys Gln
      290                    295                    300
      Ala Gly Phe Ser His Ala Pro Lys Trp Asn Thr Cys Thr Val Met Leu
      305                    310                    315                    320
      Phe Trp Trp Asn Leu Gln Val Met Phe Met Tyr Lys Ala Thr Ile Asp
                    325                    330                    335
      Gln Asn Arg Asn Tyr His Leu Ile Ser Ile Leu Pro Cys Phe Lys Lys
              340                    345                    350
      Lys Lys Lys
              355


              <210> 19
              <211> 796
              <212> DNA
              <213> Glycine max

              <220>
              <221> CDS
              <222> (1)...(513)

              <400> 19
      gca cga gca atg gcg gga gtg agg gaa cag gac cag tac atg ccg ata      48
      Ala Arg Ala Met Ala Gly Val Arg Glu Gln Asp Gln Tyr Met Pro Ile
      1               5                   10                  15

      gcg aac gtg ata agg atc atg cgt cgg att ctg cca gcg cac gcg aag      96
      Ala Asn Val Ile Arg Ile Met Arg Arg Ile Leu Pro Ala His Ala Lys
                      20                  25                  30

      atc tca gac gac gcg aag gag acg atc cag gag tgc gtg tct gag tac      144
      Ile Ser Asp Asp Ala Lys Glu Thr Ile Gln Glu Cys Val Ser Glu Tyr
                  35                  40                  45

      atc agt ttc atc acg gcg gag gcg aac gag cgg tgc cag cgg gag cag      192
      Ile Ser Phe Ile Thr Ala Glu Ala Asn Glu Arg Cys Gln Arg Glu Gln
              50                  55                  60

      cgg aag acg gtg acc gca gag gat gtg ttg tgg gcg atg gag aag ctt      240
      Arg Lys Thr Val Thr Ala Glu Asp Val Leu Trp Ala Met Glu Lys Leu
      65                  70                  75                  80

      ggc ttt gac aac tac gct cac cct ctc tct ctt tac ctt cac cgc tac      288
      Gly Phe Asp Asn Tyr Ala His Pro Leu Ser Leu Tyr Leu His Arg Tyr
```

16

```
cgc gag agt gaa gga gaa cct gct tct gtc aga cgc gct tct tct gca        336
Arg Glu Ser Glu Gly Glu Pro Ala Ser Val Arg Arg Ala Ser Ser Ala
            100             105             110

atg ggg atc aat aat aat atg gtg cac cca cct tat att aat tct cat        384
Met Gly Ile Asn Asn Asn Met Val His Pro Pro Tyr Ile Asn Ser His
            115             120             125

ggc ttt gga atg ttt gat ttt gac cca tca tcg caa ggg ttt tac agg       432
Gly Phe Gly Met Phe Asp Phe Asp Pro Ser Ser Gln Gly Phe Tyr Arg
            130             135             140

gac gat cat aac gct gct tct gga tct ggt ggt ttt gtt gcg cct ttt       480
Asp Asp His Asn Ala Ala Ser Gly Ser Gly Gly Phe Val Ala Pro Phe
145             150             155             160

gat cct tat gct aac atc aaa cgt gat gcc ctg tgatcatgta agaacaacaa     533
Asp Pro Tyr Ala Asn Ile Lys Arg Asp Ala Leu
                165             170

ctagtgcatg ctgctttttc acttggttag ttatattcaa gcacaagcac atgcaggtgc     593
agctgcaact atttagcttc atctacaaat cttttttcct ctcttcttct catgctttaa     653
ttatttagag acaatacttg ttattcattg ttatgctcaa ttgctagctt ctattcatcg     713
tcgactgtct gtattgttga tgttcattac agtaacagat aagatggtaa ctgctttact     773
acttcaaaaa aaaaaaaaaa aaa                                             796
```

```
        <210> 20
        <211> 171
        <212> PRT
        <213> Glycine max


        <400> 20
Ala Arg Ala Met Ala Gly Val Arg Glu Gln Asp Gln Tyr Met Pro Ile
1               5               10              15
Ala Asn Val Ile Arg Ile Met Arg Arg Ile Leu Pro Ala His Ala Lys
            20              25              30
Ile Ser Asp Asp Ala Lys Glu Thr Ile Gln Glu Cys Val Ser Glu Tyr
        35              40              45
Ile Ser Phe Ile Thr Ala Glu Ala Asn Glu Arg Cys Gln Arg Glu Gln
    50              55              60
Arg Lys Thr Val Thr Ala Glu Asp Val Leu Trp Ala Met Glu Lys Leu
65              70              75              80
Gly Phe Asp Asn Tyr Ala His Pro Leu Ser Leu Tyr Leu His Arg Tyr
                85              90              95
Arg Glu Ser Glu Gly Glu Pro Ala Ser Val Arg Arg Ala Ser Ser Ala
            100             105             110
Met Gly Ile Asn Asn Asn Met Val His Pro Pro Tyr Ile Asn Ser His
            115             120             125
Gly Phe Gly Met Phe Asp Phe Asp Pro Ser Ser Gln Gly Phe Tyr Arg
            130             135             140
Asp Asp His Asn Ala Ala Ser Gly Ser Gly Gly Phe Val Ala Pro Phe
145             150             155             160
Asp Pro Tyr Ala Asn Ile Lys Arg Asp Ala Leu
                165             170
```

<210> 21
<211> 1098
<212> DNA
<213> Triticum aestivum

<220>
<221> CDS
<222> (55)...(894)

<400> 21
gcacgagcaa gtgcgagtgc gactacctgc attgcacctt ggctagccct agac atg   57
                                                                    Met
                                                                    1

gag aac gac ggc gtc ccc aac gga cca gcg gcg ccg gca cct acc cag   105
Glu Asn Asp Gly Val Pro Asn Gly Pro Ala Ala Pro Ala Pro Thr Gln
            5   10   15

ggg acg ccg gtg gtg cgg gag cag gac cgg ctg atg ccg atc gcg aac   153
Gly Thr Pro Val Val Arg Glu Gln Asp Arg Leu Met Pro Ile Ala Asn
            20   25   30

gtg atc cgc atc atg cgc cgt gcg ctc cct gcc cac gcc aag atc tcc   201
Val Ile Arg Ile Met Arg Arg Ala Leu Pro Ala His Ala Lys Ile Ser
        35   40   45

gac gac gcc aag gag gcg att cag gaa tgc gtg tcc gag ttc atc agc   249
Asp Asp Ala Lys Glu Ala Ile Gln Glu Cys Val Ser Glu Phe Ile Ser
    50   55   60   65

ttc gtc acc ggc gag gcc aac gaa cgg tgc cgc atg cag cac cgc aag   297
Phe Val Thr Gly Glu Ala Asn Glu Arg Cys Arg Met Gln His Arg Lys
                70   75   80

acc gtc aac gcc gaa gac atc gtg tgg gcc cta aac cgc ctc ggc ttc   345
Thr Val Asn Ala Glu Asp Ile Val Trp Ala Leu Asn Arg Leu Gly Phe
                85   90   95

gac gac tac gtc gtg ccc ctc agc gtc ttc ctg cac cgc atg cgc gac   393
Asp Asp Tyr Val Val Pro Leu Ser Val Phe Leu His Arg Met Arg Asp
            100   105   110

ccc gag gcg ggg aca ggt ggt gcc gct gca ggc gac agc cgc gcc gtg   441
Pro Glu Ala Gly Thr Gly Gly Ala Ala Ala Gly Asp Ser Arg Ala Val
            115   120   125

acg agt gcg cct ccc cgc gcg gcc ccg ccc gtg atc cac gcc gtg ccg   489
Thr Ser Ala Pro Pro Arg Ala Ala Pro Pro Val Ile His Ala Val Pro
130   135   140   145

ctg cag gct cag cgc ccg atg tac gcg ccc ccg gct ccg ttg cag gtt   537
Leu Gln Ala Gln Arg Pro Met Tyr Ala Pro Pro Ala Pro Leu Gln Val
                150   155   160

gag aat cag atg cag cgg cct gtg tac gct ccc ccg gct ccg gtg cag   585

18

```
          Glu Asn Gln Met Gln Arg Pro Val Tyr Ala Pro Pro Ala Pro Val Gln
                      165             170             175

          gtt cag atg cag cgg ggc atc tat ggg ccc cgg gct cca gtg cac ggg      633
          Val Gln Met Gln Arg Gly Ile Tyr Gly Pro Arg Ala Pro Val His Gly
                      180             185             190

          tac gcc gtc gga atg gcg ccc gtg cgg gcc aac gtc ggc ggg cag tac      681
          Tyr Ala Val Gly Met Ala Pro Val Arg Ala Asn Val Gly Gly Gln Tyr
                      195             200             205

          cag gtg ttc ggc gga gag ggt gtc atg gcc cag caa tac tac ggg tac      729
          Gln Val Phe Gly Gly Glu Gly Val Met Ala Gln Gln Tyr Tyr Gly Tyr
          210             215             220             225

          ggg tac gag gaa gga gcg tac ggc gca ggt agc agc aac gga gga gcc      777
          Gly Tyr Glu Glu Gly Ala Tyr Gly Ala Gly Ser Ser Asn Gly Gly Ala
                      230             235             240

          gcc att ggc gac gag gag agc tcg tcc aac ggc gtg ccg gca ccg ggg      825
          Ala Ile Gly Asp Glu Glu Ser Ser Ser Asn Gly Val Pro Ala Pro Gly
                      245             250             255

          gag ggc atg ggg gag cca gag cca gag cca gca gca gaa gaa tcg cat      873
          Glu Gly Met Gly Glu Pro Glu Pro Glu Pro Ala Ala Glu Glu Ser His
                      260             265             270

          gac aag ccc gtc caa tct ggc tagtcgcgtg cgcggcgcgc gttagcttct         924
          Asp Lys Pro Val Gln Ser Gly
                      275             280

          gcgtcctgtg tactgtaata atttgccgtg tcgatccggc catggtttgt gtgtgcgtag    984
          tgcttatcta atgtgggctt gtcctctagt aattcatgta ttgcttatct aatgtggact  1044
          tgtcctctag taattcatgt actctttgct gttgaaaaaa aaaaaaaaaa aaaa         1098

              <210> 22
              <211> 280
              <212> PRT
              <213> Triticum aestivum

              <400> 22
          Met Glu Asn Asp Gly Val Pro Asn Gly Pro Ala Ala Pro Ala Pro Thr
          1               5                  10                  15
          Gln Gly Thr Pro Val Val Arg Glu Gln Asp Arg Leu Met Pro Ile Ala
                      20                  25                  30
          Asn Val Ile Arg Ile Met Arg Arg Ala Leu Pro Ala His Ala Lys Ile
                      35                  40                  45
          Ser Asp Asp Ala Lys Glu Ala Ile Gln Glu Cys Val Ser Glu Phe Ile
                      50                  55                  60
          Ser Phe Val Thr Gly Glu Ala Asn Glu Arg Cys Arg Met Gln His Arg
          65                  70                  75                  80
          Lys Thr Val Asn Ala Glu Asp Ile Val Trp Ala Leu Asn Arg Leu Gly
                      85                  90                  95
          Phe Asp Asp Tyr Val Val Pro Leu Ser Val Phe Leu His Arg Met Arg
                      100                 105                 110
          Asp Pro Glu Ala Gly Thr Gly Gly Ala Ala Ala Gly Asp Ser Arg Ala
```

19

```
                  115                    120                        125
    Val Thr Ser Ala Pro Pro Arg Ala Ala Pro Pro Val Ile His Ala Val
        130                     135                    140
    Pro Leu Gln Ala Gln Arg Pro Met Tyr Ala Pro Pro Ala Pro Leu Gln
    145                     150                    155                160
    Val Glu Asn Gln Met Gln Arg Pro Val Tyr Ala Pro Pro Ala Pro Val
                        165                     170                    175
    Gln Val Gln Met Gln Arg Gly Ile Tyr Gly Pro Arg Ala Pro Val His
                    180                     185                    190
    Gly Tyr Ala Val Gly Met Ala Pro Val Arg Ala Asn Val Gly Gly Gln
                195                     200                    205
    Tyr Gln Val Phe Gly Gly Glu Gly Val Met Ala Gln Gln Tyr Tyr Gly
        210                     215                    220
    Tyr Gly Tyr Glu Glu Gly Ala Tyr Gly Ala Gly Ser Ser Asn Gly Gly
    225                     230                    235                240
    Ala Ala Ile Gly Asp Glu Glu Ser Ser Ser Asn Gly Val Pro Ala Pro
                        245                     250                    255
    Gly Glu Gly Met Gly Glu Pro Glu Pro Glu Pro Ala Ala Glu Glu Ser
                    260                     265                    270
    His Asp Lys Pro Val Gln Ser Gly
                275                     280
```

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        <210> 23
        <211> 65
        <212> PRT
        <213> Artificial Sequence

        <220>
        <223> LEC1 consensus protein sequence

        <221> VARIANT
        <222> (1)...(65)
        <223> Xaa = Any Amino Acid

        <400> 23
    Arg Glu Gln Asp Xaa Xaa Met Pro Ile Ala Asn Val Ile Arg Ile Met
    1                   5                   10                      15
    Arg Xaa Xaa Leu Pro Xaa His Ala Lys Ile Ser Asp Asp Ala Lys Glu
                20                      25                      30
    Xaa Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Xaa Thr Xaa Glu
            35                      40                      45
    Ala Asn Xaa Arg Cys Xaa Xaa Xaa Xaa Arg Lys Thr Xaa Xaa Xaa Glu
        50                      55                      60
    Xaa
    65


        <210> 24
        <211> 36
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> Sal-A20 oligo

        <400> 24
    tcgacccacg cgtccgaaaa aaaaaaaaaa aaaaaa                            36
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<210> 25
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer-forward

<400> 25
cgctctgtca cctgttgtac tc                                          22

<210> 26
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer-reverse

<400> 26
cgtgatgaag ctgatgtact cc                                          22
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